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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 14:21:24 ; Search time 126 Seconds

(without alignments)  
7557,903 Million cell updates/sec

Title: US-09-943-075A-1\_COPY\_115\_1830

Perfect score: 1716

Sequence: 1 atggaagatctctcgcgggggt.....aggacaagccatgatgctc 1716

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database :

Issued Patents NA.\*  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1512	88.1	2303	4	US-09-197-970B-4
2	79	4.6	190	1	US-09-985-799-95
3	79	4.6	190	1	US-08-594-031-95
4	79	4.6	217	1	US-09-985-799-112
5	79	4.6	217	1	US-08-594-031-112
6	79	4.6	223	1	US-09-985-799-116
7	79	4.6	223	1	US-08-594-031-116
8	79	4.6	260	1	US-09-985-799-119
9	79	4.6	260	1	US-08-594-031-119
10	79	4.6	262	1	US-09-985-799-93
11	79	4.6	262	1	US-08-594-031-93
12	79	4.6	266	1	US-09-985-799-121
13	79	4.6	266	1	US-08-594-031-121
14	79	4.6	335	1	US-09-985-799-92
15	79	4.6	335	1	US-08-594-031-92
16	79	4.6	335	1	US-09-985-799-96
17	79	4.6	335	1	US-08-594-031-96
18	79	4.6	335	1	US-09-985-799-123
19	79	4.6	335	1	US-08-594-031-123
20	79	4.6	335	1	US-08-594-031-96
21	79	4.6	335	1	US-08-594-031-123
22	79	4.6	473	1	US-09-985-799-115
23	79	4.6	473	1	US-08-594-031-115
24	79	4.6	620	1	US-09-985-799-113
25	79	4.6	620	1	US-08-594-031-113
26	79	4.6	2213	3	US-09-383-586-27
27	59	3.4	335	1	US-09-985-799-111

28	59	3.4	335	1	US-08-594-031-111	Sequence 111, App
29	59	3.4	354	1	US-09-985-799-114	Sequence 114, App
30	59	3.4	354	1	US-08-594-031-114	Sequence 114, App
31	41	2.4	232	1	US-09-985-799-107	Sequence 107, App
32	41	2.4	232	1	US-08-594-031-107	Sequence 107, App
33	41	2.4	524	1	US-09-985-799-105	Sequence 105, App
34	41	2.4	524	1	US-08-594-031-105	Sequence 105, App
35	38	2.2	240	1	US-09-985-799-118	Sequence 118, App
36	38	2.2	240	1	US-08-594-031-118	Sequence 118, App
37	33	1.9	2669	1	US-09-985-799-91	Sequence 91, App
38	33	1.9	2669	1	US-08-594-031-91	Sequence 91, App
39	33	1.9	2669	1	US-08-594-031-91	Sequence 91, App
40	33	1.9	2669	1	US-08-594-031-101	Sequence 101, App
41	27	1.6	224	1	US-09-985-799-122	Sequence 122, App
42	27	1.6	224	1	US-08-594-031-122	Sequence 122, App
43	27	1.6	231	1	US-09-985-799-120	Sequence 120, App
44	27	1.6	231	1	US-08-594-031-120	Sequence 120, App
45	27	1.6	247	1	US-09-985-799-117	Sequence 117, App

#### ALIGNMENTS

RESULT 1  
US-09-197-970B-4  
Sequence 4, Application US/09197970B  
Patent No. 6664385  
GENERAL INFORMATION:  
APPLICANT: Michele Sanicola-Nadel  
Joseph V. Bonventre  
Catherine A. Heesslon  
Takaharu Ichimura  
Henry Wei  
Richard L. Cate  
TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Biogen, Inc.  
STREET: 14 Cambridge Center  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA  
ZIP: 02142  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,970B  
FILING DATE: 23-May-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/018,228  
FILING DATE: 24-May-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Levine, Leslie M.  
REGISTRATION NUMBER: 35,245  
REFERENCE/DOCKET NUMBER: A010 PCT CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 679-2810  
TELEFAX: (617) 679-2838  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 107..1822  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-197-970B-4

Query Match 88.1%; Score 1512; DB 4; Length 2303;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1712; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGAAGTCTCTGCGGGGCTCTGATTTCTGCTGCTGAGGAGATGCGGCTCAG 60  
DB 107 ATGGAAGTCTCTGCGGGGCTCTGATTTCTGCTGCTGAGGAGATGCGGCTCAG 166  
QY 61 GCGGCAAGCGGTTCCGTGATGCTGCGGCAATGAGCAGTATCCGATCACTAGGAG 120  
DB 167 GCGGCAAGCGGTTCCGTGATGCTGCGGCAATGAGCAGTATCCGATCACTAGGAG 226  
QY 121 AACAAACAATTACGTGGCTGCTCTTCAAGATGAATGAATGAGTGAACAGCTATCCA 180  
DB 227 AACAAACAATTACGTGGCTGCTCTTCAAGATGAATGAATGAGTGAACAGCTATCCA 286  
QY 181 GTGTGAGAGAGGAG 240  
DB 287 GTGTGAG 346  
QY 241 GCGCTAACCAAGTATCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
DB 347 GCGCTAACCAAGTATCACTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 406  
QY 301 GTGTGAG 360  
DB 407 GTGTGAG 466  
QY 361 AGAAGTATTTGAG 420  
DB 467 AGAAGTATTTGAG 526  
QY 421 SATGAG 480  
DB 527 SATGAG 586  
QY 481 CCTTCCCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540  
DB 587 CCTTCCCTGCGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 646  
QY 541 GGTGAGATTTTGAAG 600  
DB 647 GGTGAGATTTTGAAG 706  
QY 601 TTGAAGATTTGCGGCTGAGTATGATGATGATGATGATGATGATGATGATGATG 660  
DB 707 TTGAAGATTTGCGGCTGAGTATGATGATGATGATGATGATGATGATGATGATG 766  
QY 661 ATTCCATCTCCAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
DB 767 ATTCCATCTCCAAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 826  
QY 721 ACCATGACAG 780  
DB 827 ACCATGACAG 886  
QY 781 ATTTCTGATGCTGCTATCAAGATCCAGTATTTCTCAACTACTGCGCATTTCC 840  
DB 887 ATTTCTGATGCTGCTATCAAGATCCAGTATTTCTCAACTACTGCGCATTTCC 946  
QY 841 TACAAGTGAAGCTTTGGGAGACACATGCGCTGTTTGTCTCAACATGACATTTGAT 900  
DB 947 TACAAGTGAAGCTTTGGGAGACACATGCGCTGTTTGTCTCAACATGACATTTGAT 1006  
QY 901 CACAGATGCTGCTCAATGAGACCTTCACTTAACTCAAGTGAAGAGAGAGAGAGAG 960  
DB 1007 CACAGATGCTGCTCAATGAGACCTTCACTTAACTCAAGTGAAGAGAGAGAGAGAG 1066  
QY 961 GAGCATGCGGCTGACACACACCTTCTGCTTCTTCTGATCTTCTGCTGCTGATCT 1020  
DB 1067 GAGCATGCGGCTGACACACACCTTCTGCTTCTTCTGATCTTCTGCTGCTGATCT 1126

QY 1021 TCGCTTACCCCAATTATCAACACTGCTCTCTTTAATGCTGCTCAAAATCC 1080  
DB 1127 TCGCTTACCCCAATTATCAACACTGCTCTCTTTAATGCTGCTCAAAATCC 1186  
QY 1081 ATGAGCTGAGAGACATTTCCAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1140  
DB 1187 ATGAGCTGAGAGACATTTCCAAATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1246  
QY 1141 GCGCATCAACAATTGATGAGAAATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1200  
DB 1247 GCGCATCAACAATTGATGAGAAATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAG 1306  
QY 1201 CGAATCCCACTGAG 1260  
DB 1307 CGAATCCCACTGAG 1366  
QY 1261 GCGCATCCCAAG 1320  
DB 1367 GCGCATCCCAAG 1426  
QY 1321 AGGATGACAG 1380  
DB 1427 AGGATGACAG 1446  
QY 1381 AATGAGTCCGAG 1440  
DB 1487 AATGAGTCCGAG 1546  
QY 1441 ACCAGCGGCTGATCTCTATCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
DB 1547 ACCAGCGGCTGATCTCTATCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1606  
QY 1501 GGTGCTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
DB 1607 GGTGCTGATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1666  
QY 1561 TACAAG 1620  
DB 1667 TACAAG 1726  
QY 1621 AAAGGCTGAGTGTGTTTCTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
DB 1727 AAAGGCTGAGTGTGTTTCTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1786  
QY 1681 AAGATCCACTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1746  
DB 1787 AAGATCCACTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1822

RESULT 2  
US-09-985-799-95/c  
Sequence 95, Application US/09985799  
Patent No. RE38392  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTT, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-No. RE38392-2001

CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 95:  
US-09-985-799-95

Query Match 4.6%; Score 79; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 5.1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 886  
DB 181 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 122

QY 887 ATCACACTTGAATCACAC 905  
DB 121 ATCACACTTGAATCACAC 103

RESULT 3  
US-08-594-031-95/c  
Sequence 95, Application US/08594031  
Patent No. 5783182  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX:  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 190 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-594-031-95

Query Match 4.6%; Score 79; DB 1; Length 190;  
Best Local Similarity 100.0%; Pred. No. 5.1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 886  
DB 181 ACTGCGCATTCTCTCAAGTGAAGTTGGGGACAACACTGGCTGTTGTCTCCACA 122

QY 887 ATCACACTTGAATCACAC 905  
DB 121 ATCACACTTGAATCACAC 103

RESULT 4  
US-09-985-799-112  
Sequence 112, Application US/09985799  
Patent No. RE38392  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-RE38392-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 112:  
US-09-985-799-112

Query Match 4.6%; Score 79; DB 1; Length 217;  
Best Local Similarity 100.0%; Pred. No. 5,1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTTCTTCAAGTGAAGTGGGACACACTGCGCTTTGTCTCCACA 886  
DB 9 ACTGCGCATTTCTTCAAGTGAAGTGGGACACACTGCGCTTTGTCTCCACA 68

QY 887 ATCACACTTGTGATCACAC 905  
DB 69 ATCACACTTGTGATCACAC 87

## RESULT 5

US-08-594-031-112  
Sequence 112, Application US/08594031  
Patent No. 5783182  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX:  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
MOLECULE TYPE: linear  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-594-031-112

Query Match 4.6%; Score 79; DB 1; Length 217;  
Best Local Similarity 100.0%; Pred. No. 5,1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTTCTTCAAGTGAAGTGGGACACACTGCGCTTTGTCTCCACA 886

DB 9 ACTGCGCATTTCTTCAAGTGAAGTGGGACACACTGCGCTTTGTCTCCACA 68  
QY 887 ATCACACTTGTGATCACAC 905  
DB 69 ATCACACTTGTGATCACAC 87

RESULT 6  
US-09-985-799-116/c

Sequence 116, Application US/09985799  
Patent No. RE38392  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-RE38392-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 116:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 223 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 116:  
US-09-985-799-116

Query Match 4.6%; Score 79; DB 1; Length 223;  
Best Local Similarity 100.0%; Pred. No. 5,1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTGCGCATTTCTTCAAGTGAAGTGGGACACACTGCGCTTTGTCTCCACA 886  
DB 178 ACTGCGCATTTCTTCAAGTGAAGTGGGACACACTGCGCTTTGTCTCCACA 119

QY 887 ATCACACTTGTGATCACAC 905  
DB 118 ATCACACTTGTGATCACAC 100

RESULT 7

US-08-594-031-116/C  
; Sequence 116, Application US/08594031  
; Patent No. 5783182  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Timothy C.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,031  
; FILING DATE: 30-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/006,838  
; FILING DATE: 16-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Remenick, James  
; REGISTRATION NUMBER: 36,902  
; REFERENCE/DOCKET NUMBER: 0A146-0110  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-639-7700  
; TELEFAX: 202-639-7890  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 116:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 223 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE:  
; ORIGINAL SOURCE:  
; US-08-594-031-116  
Query Match 4.6%; Score 79; DB 1; Length 223;  
Best Local Similarity 100.0%; Pred. No. 5.1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 827 ACTGCGCATTTCTCAAGTGAACCTTTGGGACAACTGGCTGTGTTCTCCACA 886  
DB 178 ACTGCGCATTTCTCAAGTGAACCTTTGGGACAACTGGCTGTGTTCTCCACA 119  
QY 887 ATCACACTTGAATCACAC 905  
DB 118 ATCACACTTGAATCACAC 100

RESULT 8  
US-09-985-799-119/C  
; Sequence 119, Application US/09985799  
; Patent No. RE38392  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Timothy C.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC

COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 119:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 260 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 119:  
US-09-985-799-119  
Query Match 4.6%; Score 79; DB 1; Length 260;  
Best Local Similarity 100.0%; Pred. No. 5.1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 827 ACTGCGCATTTCTCAAGTGAACCTTTGGGACAACTGGCTGTGTTCTCCACA 886  
DB 178 ACTGCGCATTTCTCAAGTGAACCTTTGGGACAACTGGCTGTGTTCTCCACA 119  
QY 887 ATCACACTTGAATCACAC 905  
DB 118 ATCACACTTGAATCACAC 100

RESULT 9  
US-08-594-031-119/C  
; Sequence 119, Application US/08594031  
; Patent No. 5783182  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, Timothy C.  
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
; NUMBER OF SEQUENCES: 175  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: BAKER & BOTTS, L.L.P.  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/594,031

```

1      FILING DATE: 30-JUN-1996
2      CLASSIFICATION: 435
3      PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: 60/006,838
5      FILING DATE: 16-NOV-1995
6      ATTORNEY/AGENT INFORMATION:
7      NAME: Remendick, James
8      REGISTRATION NUMBER: 36,902
9      REFERENCE/DOCKET NUMBER: 0A146-0110
10     TELECOMMUNICATION INFORMATION:
11     TELEPHONE: 202-639-7700
12     TELEFAX: 202-639-7890
13     TELETYPE:
14     INFORMATION FOR SEQ ID NO: 119:
15     SEQUENCE CHARACTERISTICS:
16     LENGTH: 260 base pairs
17     TYPE: nucleic acid
18     STRANDEDNESS: single
19     TOPOLOGY: linear
20     MOLECULE TYPE: cDNA
21     HYPOTHEetical: NO
22     ANTI-SENSE: NO
23     FRAGMENT TYPE:
24     ORIGINAL SOURCE:
25     JS-08-594-031-119

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Query Match	4.6%	Score 79;	DB 1;	Length 260;
Best Local Similarity	100.0%;	Pred. No. 5.1e-30;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy		827	ACGTGCGATTTTCCTCAAGATGGAACTTTGGGAACAACACTGCCTGTTTGTCTCACA	888
Dy		178	ACGTGCGATTTTCCTCAAGATGGAACTTTGGGAACAACACTGCCTGTTTGTCTCACA	119
Oy		867	ATCACACTTTGATATACAC	905
Dy		118	ATCACACTTTGATATACAC	100

RESULT 10  
US-09-985-799-93  
; Sequence 93, Application US/09985799  
; Patent No. RE38392  
; GENERAL INFORMATION:

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84

ADDRESS: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W  
CITY: Washington

STATE: DC  
COUNTRY: USA

ZIP: 20004-2400  
COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

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; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/985,799

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FILING DATE: 06-NO. RE38392-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James  
REGISTRATION NUMBER: 36.902

REFERENCE/DOCKET NUMBER: 0A146-0110

TELEPHONE: 202-639-7700  
 TELEFAX: 202-639-7890  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 93:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 262 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: <Unknown>  
 ORIGINAL SOURCE:  
 SEQUENCE DESCRIPTION: SEQ ID NO: 93:  
 US-09-985-799-93

Query Match	4.6%	Score 79;	DB 1;	Length 262;
Best Local Similarity	100.0%;	Pred. No. 5.1e-30;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	887	ATCACACTTTGAATCACAC	905
Dib	215	ATCACACTTTGAATCACAC	233

RESULT 11  
US-08-594-031-93  
; Sequence 93, Application US/08594031

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1  GENERAL INFORMATION:
2  APPLICANT: THOMPSON, Timothy C.
3  TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
4  NUMBER OF SEQUENCES: 175
5  CORRESPONDENCE ADDRESS:

```

ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W  
;

; CITY: Washington  
; STATE: DC  
;

COUNTRY: USA  
ZIP: 20004-2400

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
;

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;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Demenick James

REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 00

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 303-638-7700

TELEPHONE: 202-639-7890  
TELEFAX: 202-639-7890  
FAX: 202-639-7890

TELEA: INFORMATION FOR SEQ ID NO: 93  
; PROTEIN CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:  
LENGTH: 262 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single

```

;          TOPOLOGY: linear
;
;          MOLECULE TYPE: cDNA
;

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ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:

Query Match  
Best Local Similarity 100.0%; Score 79; DB 1; Length 262;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGCGCTGTTGTCTCCACA 886  
DB 155 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGCGCTGTTGTCTCCACA 214  
QY 887 ATCACACTTTGAATCACAC 905  
DB 215 ATCACACTTTGAATCACAC 233

## RESULT 12

US-09-985-799-121/c  
Sequence 121, Application US/09985799  
Patent No. RE38392

GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890

TELEFAX: 202-639-7890  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 121:  
US-09-985-799-121

Query Match  
Best Local Similarity 100.0%; Score 79; DB 1; Length 286;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGCGCTGTTGTCTCCACA 886  
DB 153 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGCGCTGTTGTCTCCACA 94  
QY 887 ATCACACTTTGAATCACAC 905  
DB 93 ATCACACTTTGAATCACAC 75

## RESULT 13

US-08-594-031-121/c  
Sequence 121, Application US/08594031  
Patent No. 5783182

GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890

TELEFAX: 202-639-7890  
INFORMATION FOR SEQ ID NO: 121:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 286 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-594-031-121

Query Match  
Best Local Similarity 100.0%; Score 79; DB 1; Length 286;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 827 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGCGCTGTTGTCTCCACA 886  
DB 153 ACTCTGCATTTCCTACAGTGAAGTGGAGCAACTGCGCTGTTGTCTCCACA 94  
QY 887 ATCACACTTTGAATCACAC 905  
DB 93 ATCACACTTTGAATCACAC 75

RESULT 14  
US-09-985-799-92  
Sequence 92, Application US/09985799

Patent No. RE38392  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 92:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 92:  
US-09-985-799-92  
Query Match 4.6%; Score 79; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5.1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 827 ACTGCGCAATTCCTCAAGTGAAGTGGGACACAGCTGGCTGTGTTCTCCACA 886  
DB 155 ACTGCGCAATTCCTCAAGTGAAGTGGGACACAGCTGGCTGTGTTCTCCACA 214  
QY 887 ATCACACTTGAATCACAC 905  
DB 215 ATCACACTTGAATCACAC 233  
RESULT 15  
US-09-985-799-94  
Sequence 94, Application US/09985799  
Patent No. RE38392  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington

STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 94:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 335 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 94:  
US-09-985-799-94  
Query Match 4.6%; Score 79; DB 1; Length 335;  
Best Local Similarity 100.0%; Pred. No. 5.1e-30;  
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 827 ACTGCGCAATTCCTCAAGTGAAGTGGGACACAGCTGGCTGTGTTCTCCACA 886  
DB 155 ACTGCGCAATTCCTCAAGTGAAGTGGGACACAGCTGGCTGTGTTCTCCACA 214  
QY 887 ATCACACTTGAATCACAC 905  
DB 215 ATCACACTTGAATCACAC 233  
Search completed: April 30, 2004, 16:17:56  
Job time : 126 secs



Result No.	Score	Query Match	Length	DB	ID	Description
1	1716	100.0	2330	1	US-09-943-075A-1	Sequence 1, Appl
2	425	24.8	631	17	US-10-404-460-129	Sequence 129, Appl
3	178	10.4	294	9	US-09-917-800A-139	Sequence 139, App
4	178	10.4	294	12	US-10-157-319A-122	Sequence 122, Appl
5	178	10.4	294	16	US-10-191-803-372	Sequence 372, App
6	79	4.6	1275	9	US-09-943-075A-7	Sequence 7, Appl
7	79	4.6	2213	9	US-09-823-038A-27	Sequence 27, Appl
8	65	3.8	65	10	US-09-908-975-1458	Sequence 1458, App
9	33	1.9	318	9	US-09-864-761-18279	Sequence 18279, A
10	33	1.9	478	9	US-09-864-761-1520	Sequence 1520, App
11	33	1.9	1393	17	US-10-309-280-153	Sequence 153, Appl
12	33	1.9	1410	17	US-10-309-280-149	Sequence 149, App
13	33	1.9	1542	17	US-10-309-280-147	Sequence 147, Appl
14	33	1.9	1683	9	US-09-943-075A-8	Sequence 8, Appl

45	33	1.9	2683	15	US-10-232-233-41	Sequence 41, Appl
44	33	1.9	2683	15	US-10-232-233-41	Sequence 41, Appl
43	33	1.9	2683	15	US-10-230-260-41	Sequence 41, Appl
42	33	1.9	2683	15	US-10-219-481-41	Sequence 41, Appl
41	33	1.9	2683	15	US-10-219-479-41	Sequence 41, Appl
40	33	1.9	2683	15	US-10-219-466-41	Sequence 41, Appl
39	33	1.9	2683	15	US-10-219-464-41	Sequence 41, Appl
38	33	1.9	2683	15	US-10-219-075-41	Sequence 41, Appl
37	33	1.9	2683	15	US-10-219-003-41	Sequence 41, Appl
36	33	1.9	2683	15	US-10-230-434-41	Sequence 41, Appl
35	33	1.9	2683	15	US-10-230-076-41	Sequence 41, Appl
34	33	1.9	2683	15	US-10-219-075-41	Sequence 41, Appl
33	33	1.9	2683	15	US-10-227-883-41	Sequence 41, Appl
32	33	1.9	2683	15	US-10-227-873-41	Sequence 41, Appl
31	33	1.9	2683	15	US-10-216-159A-41	Sequence 41, Appl
30	33	1.9	2683	15	US-10-218-631-41	Sequence 41, Appl
29	33	1.9	2683	15	US-10-230-414-41	Sequence 41, Appl
28	33	1.9	2683	15	US-10-330-138-41	Sequence 41, Appl
27	33	1.9	2683	15	US-10-330-163-41	Sequence 41, Appl
26	33	1.9	2683	15	US-10-327-884-41	Sequence 41, Appl
25	33	1.9	2683	13	US-10-232-230-41	Sequence 41, Appl
24	33	1.9	2683	13	US-10-232-224-41	Sequence 41, Appl
23	33	1.9	2683	13	US-10-219-535-41	Sequence 41, Appl
22	33	1.9	2669	16	US-10-295-027-1041	Sequence 1041, Appl
21	33	1.9	2669	13	US-10-172-118-779	Sequence 779, Appl
20	33	1.9	2669	13	US-10-342-887-779	Sequence 779, Appl
19	33	1.9	2669	10	US-09-525-978B-82	Sequence 82, Appl
18	33	1.9	2669	15	US-10-084-817-169	Sequence 169, Appl
17	33	1.9	2661	14	US-10-039-272-1	Sequence 1, Appl
16	33	1.9	2653	17	US-10-363-106-1	Sequence 151, Appl
15	33	1.9	1923	17	US-10-309-290-151	Sequence 151, Appl

## ALIGNMENTS

```

1      RESULT 1
2      US-09-943-075A-1
3      : Sequence 1, Application US/09943075A
4      : Patent No. US20020151486A1
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Popoff, Steven N.
9      : APPLICANT: Safado, Fayer F.
10     : APPLICANT: Owen, Thomas A.
11     : APPLICANT: Smock, Steven L.
12     :
13     : TITLE OF INVENTION: Osteocalcin Protein and Methods of Stimulating Bone Differentiation
14     :
15     : FILE REFERENCE: 71369,262
16     :
17     : CURRENT APPLICATION NUMBER: US/09/943,075A
18     :
19     : CURRENT FILING DATE: 2001-08-30
20     :
21     : PRIOR APPLICATION NUMBER: US 60/229,006
22     :
23     : PRIOR FILING DATE: 2000-08-30
24     :
25     : NUMBER OF SEQ. ID NOS: 8
26     :
27     : SOFTWARE: FastSeq for Windows Version 4.0
28     :
29     : SEQ ID NO 1
30     :
31     : LENGTH: 2320
32     :
33     : TYPE: DNA
34     :
35     : ORGANISM: Rat osteocalcin
36     :
37     : FEATURE:
38     :
39     : NAME/KEY: CDS
40     :
41     : LOCATION: (115)...(1833)
42     :
43     : US-09-943-075A-1

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Query Match	100.0%	Score 1716;	DB 9;	Length 2320;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1716;	Conservative 0;	Mismatched 0;	Indels 0;	Gaps 0

  

QY	1	ATGAAAGTCTCTGGGGGCTCTGATTTCTCTGCTGGAGACTGCGCTCCAG	60
DB	115	ATGAAAGTCTCTGGGGGCTCTGATTTCTCTGCTGGAGACTGCGCTCCAG	174
QY	61	CGGCTCAACGGTTCCGTATTCCTGGGCGCAGACATATCCGATATCAGAGGAG	120

Db 175 GGGGCAAGCGGTTCCGATGATGCTGGGCAATGACAGTATCCGGATCAATGAGGAG 234  
Qy 121 AACACCAATTAAGTGGCTGTCTTCAAGATGAATAATGAATGAGTGAACAGCTGTATCCA 180  
Db 235 AACAAACCAATTAAGTGGCTGTCTTCAAGATGAATAATGAATGAGTGAACAGCTGTATCCA 294  
Qy 181 GTGTGAG 240  
Db 295 GTGTGAG 354  
Qy 241 GGCCTAACCAAGTATTCACCGGCTGTGGTGGTTCATATCACTTCCAGTGAACCTG 300  
Db 355 GGCCTAACCAAGTATTCACCGGCTGTGGTGGTTCATATCACTTCCAGTGAACCTG 414  
Qy 301 GTGTTCCTCCAGATGCCAAGAGAGATGCCAAGAGATGCCAAGAGATGCCAAGAGATGCC 360  
Db 415 GTGTTCCTCCAGATGCCAAGAGAGATGCCAAGAGATGCCAAGAGATGCCAAGAGATGCC 474  
Qy 361 AAGAGTGAATTTGAGAGCTGGCTTGCAGCCGATATGCTCACTGAGCAACAGAGGAGAGAC 420  
Db 475 AAGAGTGAATTTGAGAGCTGGCTTGCAGCCGATATGCTCACTGAGCAACAGAGGAGAGAC 534  
Qy 421 GATGAGAGCTGGAGAGCAACACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
Db 535 GATGAGAGCTGGAGAGCAACACAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 594  
Qy 481 CCTTCCCTCCAG 540  
Db 595 CCTTCCCTCCAG 654  
Qy 541 GGTCAAGTATTTTCAAAAGCTGGGTGAGTTCAGACAGAGTTCATATTAACAGAGTCAAC 600  
Db 655 GGTCAAGTATTTTCAAAAGCTGGGTGAGTTCAGACAGAGTTCATATTAACAGAGTCAAC 714  
Qy 601 TTGACAGTTGGCCCTCAAGTCAATGAGAGATGTTCTTTCGAGAGACAGGCGCGAGTAC 660  
Db 715 TTGACAGTTGGCCCTCAAGTCAATGAGAGATGTTCTTTCGAGAGACAGGCGCGAGTAC 774  
Qy 661 ATTCCCATCTCCAAAGTGAAG 720  
Db 775 ATTCCCATCTCCAAAGTGAAG 834  
Qy 721 ACCATGTACAGAGAGATGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
Db 835 ACCATGTACAGAGAGATGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 894  
Qy 781 ATTTCTTCATGATGCTCATTCACATCCAGTCCATTTCTTCAACATGCTGCAATTTCC 840  
Db 895 ATTTCTTCATGATGCTCATTCACATCCAGTCCATTTCTTCAACATGCTGCAATTTCC 954  
Qy 841 TACAAATGGAATTTGGGAGCAACAGCTGGCTGTGTTGCTTCACAAATCACTCTTGAAAT 900  
Db 955 TACAAATGGAATTTGGGAGCAACAGCTGGCTGTGTTGCTTCACAAATCACTCTTGAAAT 1014  
Qy 901 CACAGTATGCTCAATGGAATCTTCACTTAACTGACAGGCAACCTGAGAGAGAGAGAGAG 960  
Db 1015 CACAGTATGCTCAATGGAATCTTCACTTAACTGACAGGCAACCTGAGAGAGAGAGAGAG 1074  
Qy 961 GAGCAGTGGCCCTCAACCAACCTTGGCTTCTTTCGATCTTCTGCTGCTGATCT 1020  
Db 1075 GAGCAGTGGCCCTCAACCAACCTTGGCTTCTTTCGATCTTCTGCTGCTGATCT 1134  
Qy 1021 TGGGCTTCCAGAGATGATGACAGTATGCTCCCTTAAAGCTGAGAGAGAGAGAGAGAGAG 1080  
Db 1135 TGGGCTTCCAGAGATGATGACAGTATGCTCCCTTAAAGCTGAGAGAGAGAGAGAGAGAG 1194  
Qy 1081 ATGAGCTGAGTGAATTTCCATGATGAATGCGAGATGAACAGATATGTTACTTCAAG 1140  
Db 1195 ATGAGCTGAGTGAATTTCCATGATGAATGCGAGATGAACAGATATGTTACTTCAAG 1254  
Qy 1141 GCCACCATCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
Db 1255 GCCACCATCAAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1314

Qy 1201 CCATTTCCCAACATGCAAGCTGATGAACTCACTGATGAACTTCAATTTGAGCTGCAAAAGG 1260  
Db 1315 CCATTTCCCAACATGCAAGCTGATGAACTCACTGATGAACTTCAATTTGAGCTGCAAAAGG 1374  
Qy 1261 GCCATCTCCAGAGAGAGCTGTACATGATCTTGAACCCACCTGAGATGAGAGAGAGAGAG 1320  
Db 1375 GCCATCTCCAGAGAGAGCTGTACATGATCTTGAACCCACCTGAGATGAGAGAGAGAGAG 1434  
Qy 1321 AAGGTGTGAG 1380  
Db 1435 AAGGTGTGAG 1494  
Qy 1381 AATGGGTCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
Db 1495 AATGGGTCCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1554  
Qy 1441 ACCAGAGCCCTGATCTGTATCCCTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
Db 1555 ACCAGAGCCCTGATCTGTATCCCTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1614  
Qy 1501 GTGTCTGATATCTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
Db 1615 GTGTCTGATATCTCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1674  
Qy 1561 TACAAAAAACAAGAGAGTACAAAGCCAAATAGAAAACTGACAGAGAGAGAGAGAGAGAGAG 1620  
Db 1675 TACAAAAAACAAGAGAGTACAAAGCCAAATAGAAAACTGACAGAGAGAGAGAGAGAGAGAG 1734  
Qy 1621 AAAAGGCTGAGTGTGTTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680  
Db 1735 AAAAGGCTGAGTGTGTTTCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1794  
Qy 1681 AAGATCCACTGCTCCAG 1716  
Db 1795 AAGATCCACTGCTCCAG 1830

## RESULT 2

US-10-404-460-129  
; Sequence 129, Application US/10404460  
; Publication No. US20040076974A1  
; GENERAL INFORMATION:  
; APPLICANT: PHASE-1 Molecular Toxicology, Inc.  
; APPLICANT: Kier, Larry  
; APPLICANT: Nolan, Timothy D.  
; APPLICANT: Sankar, Uma  
; APPLICANT: Derbel, Maher  
; TITLE OF INVENTION: Liver Necrosis Predictive Genes  
; FILE REFERENCE: 2874-022  
; CURRENT APPLICATION NUMBER: US/10/404,460  
; CURRENT FILING DATE: 2003-04-01  
; PRIOR APPLICATION NUMBER: US 60/369,287  
; PRIOR FILING DATE: 2002-04-01  
; NUMBER OF SEQ ID NOS: 266  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 129  
; LENGTH: 631  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: predictive genes for liver necrosis  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 2, 589, 626  
; OTHER INFORMATION: n = A,T,C or G  
US-10-404-460-129

Query Match 24.8%; Score 425; DB 17; Length 631;  
Best Local Similarity 100.0%; Pred. No. 5.9e-214;  
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAGAAAGTCTCGGAGGCTCTGATTTCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 60

Db 153 ATGGAAAGTCTGCGGGGCTCTGGAATTTCTGCTGCTGCATGAGACCTGCCCTCCAG 222  
Qy 61 GCGGCCAAGGCGGTTCCGATGATGTCCTGAGCATGAGCATGATCCGATCATGAGGAG 120  
Db 223 GCGGCCAAGGCGGTTCCGATGATGTCCTGAGCATGAGCATGATCCGATCATGAGGAG 282  
Qy 121 AACAAACCAATTAGCTGCTGCTCTTCAGTAAATGATGAGATGAAACAGCTGTATCCA 180  
Db 283 AACAAACCAATTAGCTGCTGCTCTTCAGTAAATGATGAGATGAAACAGCTGTATCCA 342  
Qy 181 GTGTGAGAGAGGAGAGAGGAGATGAGAGACTCTTGGAGAGAGAGCCGTGTGACGCA 240  
Db 343 GTGTGAGAGAGGAGAGAGGAGATGAGAGACTCTTGGAGAGAGAGCCGTGTGACGCA 402  
Qy 241 GCGCCTAACAGTATTCACCGGCTTGTGAGGCTTCAATATACCTTGTGATGAGACTG 300  
Db 403 GCGCCTAACAGTATTCACCGGCTTGTGAGGCTTCAATATACCTTGTGATGAGACTG 462  
Qy 301 GTGTTCCTCCAGATGCCAGAGAGAGATGCCAAGGCAATATCTGTATGAGAGACTGC 360  
Db 463 GTGTTCCTCCAGATGCCAGAGAGAGATGCCAAGGCAATATCTGTATGAGAGACTGC 522  
Qy 361 AGAAGTATTTGAGAGCTGCTTCTGACCCGTATGCTCAACTGAGACCAAGGCGACAC 420  
Db 523 AGAAGTATTTGAGAGCTGCTTCTGACCCGTATGCTCAACTGAGACCAAGGCGACAC 582  
Qy 421 GATGA 425  
Db 583 GATGA 587

## RESULT 3

US-09-917-800A-139/c

Sequence 139, Application US/09917800A

Patent No. US20020119462A1

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

APPLICANT: Porter, Mark

APPLICANT: Johnson, Kory

APPLICANT: Castle, Arthur

APPLICANT: Blashoff, Michael

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5038-US

CURRENT APPLICATION NUMBER: US/09/917,800A

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/222,040

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: US 60/222,880

PRIOR FILING DATE: 2000-11-02

PRIOR APPLICATION NUMBER: US 60/290,029

PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/290,645

PRIOR FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: US 60/292,336

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 60/295,798

PRIOR FILING DATE: 2001-06-06

PRIOR APPLICATION NUMBER: US 60/297,457

PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,884

PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,459

PRIOR FILING DATE: 2001-07-09

NUMBER OF SEQ ID NOS: 1740

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 139

LENGTH: 294

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA851814

US-09-917-800A-139

Query Match

10.4%; Score 178; DB 9; Length 294;

Best Local Similarity 100.0%; Pred. No. 3.4e-83;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1075 AATTCATGAGCTGAGTGCATTTCCATGAAACTCCGAAATTAACGATATGTTAC 1134

Db 294 AATTCATGAGCTGAGTGCATTTCCATGAAACTCCGAAATTAACGATATGTTAC 235

Qy 1135 TTCAGAGCCACATCCATCTGATGATGATCTTGAAGTCAATCATCTCAGGTAGCA 1194

Db 234 TTCAGAGCCACATCCATCTGATGATGATCTTGAAGTCAATCATCTCAGGTAGCA 175

Qy 1195 GATGTCCCAATCCCACTGTGAGCTGACCACTGATGAGCTTCAATGTGACT 1252

Db 174 GATGTCCCAATCCCACTGTGAGCTGACCACTGATGAGCTTCAATGTGACT 117

## RESULT 4

US-10-152-319A-122/c

Sequence 122, Application US/10152319A

Publication No. US20040072160A1

GENERAL INFORMATION:

APPLICANT: Mendrick, Donna

APPLICANT: Porter, Mark

APPLICANT: Johnson, Kory

APPLICANT: Higgs, Brandon

APPLICANT: Castle, Arthur

APPLICANT: Blashoff, Michael

TITLE OF INVENTION: Molecular Toxicology Modeling

FILE REFERENCE: 44921-5089-US

CURRENT APPLICATION NUMBER: US/10/152,319A

CURRENT FILING DATE: 2002-05-22

PRIOR APPLICATION NUMBER: US 60/292,335

PRIOR FILING DATE: 2001-05-22

PRIOR APPLICATION NUMBER: US 60/297,523

PRIOR FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: US 60/298,925

PRIOR FILING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: US 60/303,810

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,807

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/303,808

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/315,047

PRIOR FILING DATE: 2001-08-28

PRIOR APPLICATION NUMBER: US 60/324,928

PRIOR FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/330,867

PRIOR FILING DATE: 2001-11-01

PRIOR APPLICATION NUMBER: US 60/330,462

PRIOR FILING DATE: 2001-10-22

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 2221

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 122

LENGTH: 294

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

OTHER INFORMATION: Genbank Accession No. AA851814

US-10-152-319A-122

Query Match 10.4%; Score 178; DB 12; Length 294;

Best Local Similarity 100.0%; Pred. No. 3.4e-83;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1075 AATTCATGAGCTGAGTGCATTTCCATGAAACTCCGAAATTAACGATATGTTAC 1134

Db 294 AATTCATGAGCTGAGTGCATTTCCATGAAACTCCGAAATTAACGATATGTTAC 235

QY 1135 TTGAGGCCACATCACAATGTAGATGGAATCTGGAAGCAACATCATCCAGTGGCA 1194

Db 234 TTCCAGGCCACATCACAATGTAGATGGAATCTGGAAGCAACATCATCCAGTGGCA 175

QY 1135 GATGTCCCAATCCCAACATGCAAGCTGCAACAATCAATGACCTTCTGTATGACT 1232

Db 174 GATGTCCCAATCCCAACATGCAAGCTGCAACAATCAATGACCTTCTGTATGACT 117

## RESULT 5

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US-10-191-803-372/c
/ Sequence 372, Application US/10191803
/ Publication No. US20040014040A1
/ GENERAL INFORMATION:
/ APPLICANT: MENDRICK, Donna
/ APPLICANT: PORTER, Mark
/ APPLICANT: JONSON, Kory
/ APPLICANT: HIGGS, Brandon
/ APPLICANT: CASTLE, Arthur
/ APPLICANT: ELASHOFF, Michael
/ TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5090US
/ CURRENT APPLICATION NUMBER: US/10/191,803
/ CURRENT FILING DATE: 2002-07-10
/ PRIOR APPLICATION NUMBER: US 60/303,819
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 60/305,623
/ PRIOR FILING DATE: 2001-07-17
/ PRIOR APPLICATION NUMBER: US 60/369,351
/ PRIOR FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: US 60/377,611
/ PRIOR FILING DATE: 2002-05-06
/ NUMBER OF SEQ ID NOS: 1140
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 372
/ LENGTH: 294
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20040014040A1 PA86181814
US-10-191-803-372

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Query Match	10.4%;	Score 178;	DB 16;	Length 294;
Best Local Similarity	100.0%;	Pred. No. 3.4e-83;		
Matches 178;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

OY	1075	AAATCATGAGACTGAGTGACATTTCCAGTGAAGAACTGGCCAAATAAAGAGATATGGTTC	1134
Db	294	AAATCCATGAGACTGAGTGACATTTCCAGTGAAGAACTGGCCAAATAAAGAGATATGGTTC	235
OY	1135	TTCCAGGCCACATCACTAATTGATGATGATCTGTGAAGTCACTCATCTCCAGGTAGCA	1194
Db	234	TTCCAGGCCACATCACTAATTGATGATGATCTGTGAAGTCACTCATCTCCAGGTAGCA	175
OY	1195	GATGTCCCAATCCCACTGACAGCCCTGACACTCACTCATGATGACATTATGTGACTT	1252
Db	174	GATGTCCCAATCCCACTGACAGCCCTGACACTCACTCATGATGACATTATGTGACTT	117

## RESULT

US-09-943-075A-7  
Sequence 7, Application US/09943075A  
Patent No. US20020151486A1  
GENERAL INFORMATION:  
APPLICANT: Popoff, Steven N.  
APPLICANT: Safado, Favez F.  
APPLICANT: Owen, Thomas A.  
APPLICANT: Smock, Steven L.  
TITLE OF INVENTION: Osteocalcin Protein and Nucleic Acids Encoding the Same,  
TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation  
FILE REFERENCE: 71369.262  
CURRENT APPLICATION NUMBER: US/09/943,075A  
CURRENT FILING DATE: 2001-08-30

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: PRIOR APPLICATION NUMBER: US 60/229,006
: PRIOR FILING DATE: 2000-08-30
: NUMBER OF SEQ. ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO. 7
: LENGTH: 1725
: TYPE: DNA
: ORGANISM: Mouse
US-09-943-075A-7

4.6%; Score 79; DB 9; Length 1725;
Best Local Similarity 100.0%; Pred. No. 8,2e-31;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	387	ACCTGTCACATTCCCAAAATGGAACTTTGGGACAAACACTG393CTTTTGTCTCAACA	386
Db	827	ACCTGTCACATTCCCAAAATGGAACTTTGGGACAAACACTG393CTTTTGTCTCAACA	836
Qy	887	ATCAACATTGATACAC	905
Db	887	ATCAACATTGATACAC	905

RESULT 7

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US-09-823-038A-27
? Sequence 27, Application US/09823038A
? Patent No. US20020058355A1
? GENERAL INFORMATION:
? APPLICANT: Strachan, Lorna
? APPLICANT: Saleman, Matthew
? APPLICANT: Abernethy, Nevlin
? APPLICANT: Ornsted, Rene
? APPLICANT: Kumble, Brand
? APPLICANT: Marleson, Greg
? TITLE OF INVENTION: Compositions Isolated From Stromal Cells
? TITLE OF INVENTION: And Methods For Their Use
? FILE REFERENCE: 11000.103763
? CURRENT APPLICATION NUMBER: US/09/823,038A
? CURRENT FILING DATE: 2001-07-09
? NUMBER OF SEQ ID NOS: 61
? SOFTWARE: FASTSEQ For Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 2213
? TYPE: DNA
? ORGANISM: Mouse
US-09-823-038A-27

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Query Match	4.6%;	Score 79;	DB 9;	Length 2213;
Best Local Similarity	100.0%;	Pred. No. 8.2e-31;		
Matches 79;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY 827 ACTGTGCACATTTCCACAAAGTGGAACTTTGGGACAACAACCTGAGCTGTGTGTCCACA 888  
DB 849 ACTGTGCATTTCCACAAAGTGGAACTTTGGGACAACAACCTGTGTGTCCACA 908  
QY 887 ATCACACTTTGAATCAGC 905  
DB 909 ATCACACTTGAATCAGC 927

## RESULT 3

```

US-09-908-975-1458
; Sequence 1458, Application US/09908975
; Publication No. US20030165843A1
;
GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Irit
; APPLICANT: FALGER, Shimon
; TITLE OF INVENTION: Oligonucleotide library for detecting RNA transcripts and splice
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005

```

CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: Patent version 3.0  
SEQ ID NO 1458  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-908-975-1458

Query Match  
Best Local Similarity 100.0%; Pred. No. 2,4e-23;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3.8%; Score 65; DB 10; Length 65;  
Best Local Similarity 100.0%; Pred. No. 2,4e-23;  
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 770 GAGACCTCCCTTTCTTGATGTCCTCATTCAGATCCGATCTTTCTCACTACT 829  
1 GAGACCTCCCTTTCTTGATGTCCTCATTCAGATCCGATCTTTCTCACTACT 60

Qy 830 CTGCC 834  
61 CTGCC 65

Db 61 CTGCC 65

RESULT 9  
US-09-864-761-18279/c  
Sequence 18279, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 18279  
LENGTH: 318  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005082.2  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 27  
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2  
OTHER INFORMATION: SWISSPROT HIT: Q14956, EVALUE 8.00e-46  
OTHER INFORMATION: EST HUMAN HIT: BE672596.1, EVALUE 0.00e+00  
OTHER INFORMATION: NT HIT: AF322909.1, EVALUE 0.00e+00  
US-09-864-761-18279

Query Match  
Best Local Similarity 1.9%; Score 33; DB 9; Length 318;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.0%; Pred. No. 2e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 896 TGAATCAGCTATGCTCTCAATGACCTTCA 928  
123 TGAATCAGCTATGCTCTCAATGACCTTCA 91

Db 123 TGAATCAGCTATGCTCTCAATGACCTTCA 91

RESULT 10  
US-09-864-761-1520/c  
Sequence 1520, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263,6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00660  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 1520  
LENGTH: 478  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC005082.2  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.9  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.6  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.7  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 27  
OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 2  
US-09-864-761-1520

Query Match 1.9%; Score 33; DB 9; Length 478;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 896 TGAATCACGATGTCCTCATGGAACCTTCA 928  
DB 319 TGAATCACGATGTCCTCATGGAACCTTCA 287

RESULT 11  
US-10-309-290-153  
Sequence 153, Application US/10309290  
Publication No. US20040023241A1  
GENERAL INFORMATION:  
APPLICANT: Alsobrook II, John P.  
APPLICANT: Anderson, David W.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Chilikuru, Rajeev A.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Gorman, Linda  
APPLICANT: Gould-Rothberg, Bonnie E.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Jeffers, Michael E.  
APPLICANT: Ji, Weizhen  
APPLICANT: Li, Li  
APPLICANT: Malysankar, Uriel M.  
APPLICANT: Miller, Charles E.  
APPLICANT: Murphey, Ryan  
APPLICANT: Patturajan, Meera  
APPLICANT: Peyman, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Smithson, Glenda  
APPLICANT: Starling, Gary  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zhong, Hailong

APPLICANT: Zhong, Mei  
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD  
FILE REFERENCE: 21402-502A  
CURRENT FILING DATE: 2002-12-02  
PRIOR FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/336,600  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: 60/338,285  
PRIOR FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 60/341,346  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/341,477  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/341,540  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/342,592  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/344,297  
PRIOR FILING DATE: 2001-12-27  
PRIOR APPLICATION NUMBER: 60/344,903  
PRIOR FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/373,288  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 60/380,981  
PRIOR FILING DATE: 2002-05-15  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 274  
SOFTWARE: CursSeqList version 0.1  
SEQ ID NO 153  
LENGTH: 1393  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)..(1393)  
US-10-309-290-153

Query Match 1.9%; Score 33; DB 17; Length 1393;  
Best Local Similarity 100.0%; Pred. No. 1.9e-06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 896 TGAATCACGATGTCCTCATGGAACCTTCA 928  
DB 840 TGAATCACGATGTCCTCATGGAACCTTCA 872

RESULT 12  
US-10-309-290-149  
Sequence 149, Application US/10309290  
Publication No. US20040023241A1  
GENERAL INFORMATION:  
APPLICANT: Alsobrook II, John P.  
APPLICANT: Anderson, David W.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Chilikuru, Rajeev A.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Gorman, Linda  
APPLICANT: Gould-Rothberg, Bonnie E.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Jeffers, Michael E.  
APPLICANT: Ji, Weizhen  
APPLICANT: Li, Li  
APPLICANT: Malysankar, Uriel M.  
APPLICANT: Miller, Charles E.  
APPLICANT: Murphey, Ryan  
APPLICANT: Patturajan, Meera  
APPLICANT: Peyman, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Rieger, Daniel K.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Smithson, Glenda

```

; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,303
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Curaseqdist version 0.1
; SEQ ID NO 149
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1410)
; US-10-309-290-149

Query Match          1.9%; Score 33; DB 17; Length 1410;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      896 TGAATCACAGTATGTGCTCATGGAACCTTCA 928
Db      830 TGAATCACAGTATGTGCTCATGGAACCTTCA 862

RESULT 13
US-10-309-290-147
; Sequence 147, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsebrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chhillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rochberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malysankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
```

```

; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel X.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,303
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: Curaseqdist version 0.1
; SEQ ID NO 147
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
; US-10-309-290-147

Query Match          1.9%; Score 33; DB 17; Length 1542;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      896 TGAATCACAGTATGTGCTCATGGAACCTTCA 928
Db      830 TGAATCACAGTATGTGCTCATGGAACCTTCA 862

RESULT 14
US-09-943-075A-8
; Sequence 8, Application US/09943075A
; Patent No. US2002015146A1
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Fayer F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
; TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
; FILE REFERENCE: 71369,262
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
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; LENGTH: 1683
; TYPE: DNA
; ORGANISM: Human
US-09-943-075A-8

Query Match          1.9%; Score 33; DB 9; Length 1683;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      896 TGAATCACACGTATGTGCTCAATGGAACCTTCA 928
Db      896 TGAATCACACGTATGTGCTCAATGGAACCTTCA 928

RESULT 15
US-10-309-290-151
; Sequence 151, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chhikara, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malvankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
CURRENT FILING DATE: 2002-12-02
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/341,540
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/380,981
PRIOR FILING DATE: 2002-05-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SOFTWARE: Curaseqlast version 0.1
```

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; SEQ ID NO 151
; LENGTH: 1923
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(1774)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: wherein n may be a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(3)
; OTHER INFORMATION: wherein n may be a, c, g or t
US-10-309-290-151

Query Match          1.9%; Score 33; DB 17; Length 1923;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      896 TGAATCACACGTATGTGCTCAATGGAACCTTCA 928
Db      990 TGAATCACACGTATGTGCTCAATGGAACCTTCA 1022

Search completed: April 30, 2004, 17:58:44
Job time : 713 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 30, 2004, 16:15:45 ; Search time 121 Seconds

(without alignments)  
2623.404 Million cell updates/sec

Title: US-09-943-075A-2

Perfect score: 572  
Sequence: 1 MBSLCGVLFVFLIANGPLPQ.....PSRGRDRKPKPLQDXPMML 572

Scoring table:

OLIGO	Xgapop 60.0	Xgapext 60.0
Ygapop 60.0	Ygapext 60.0	Pgapop 6.0
Pgapext 7.0	Delop 6.0	Delext 7.0

Searched: 682709 segs, 277475446 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1360453

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-MODE=frame+ p2n.model -DEV=xip  
-O=/cgn2_1/USPTO.spool/p/US09943075/rnat.29042004.162536.5965/app.query.fasta_1.711  
-DB-Issued Patents NA -OPMT=fastap -SUPPLX=clip2n.rml -MINMATCH=0.1 -LOOPECL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=humand4.cdd  
-LIST=45 -DOCALIGN=200 -THR.SCOR=quality -THR.MIN=1 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09943075.@CGN 1 1 103 @rnat.29042004.162536.5965 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG.SCOR=0 -WAIT -DSPELCK=100 -LONGLOG  
-DEV TIMEOUT=120 -NARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -YGAPOP=6  
-YGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Database :

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1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*  
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*  
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*  
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*  
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:*  
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	181	31.6	2303	4	US-09-197-970B-4
2	43	7.5	335	1	US-09-985-799-111
3	43	7.5	335	1	US-08-594-031-111
4	43	7.5	354	1	US-09-985-799-114
5	43	7.5	354	1	US-08-594-031-114
6	43	7.5	473	1	US-09-985-799-115
7	43	7.5	473	1	US-08-594-031-115
8	43	7.5	620	1	US-09-985-799-113
9	43	7.5	620	1	US-08-594-031-113
10	43	7.5	2213	3	US-09-983-586-27
11	36	6.3	240	1	US-09-985-799-118
12	36	6.3	240	1	US-08-594-031-118

C 13	34	5.9	190	1	US-09-985-799-95	Sequence 95, App1
C 14	34	5.9	190	1	US-08-594-031-95	Sequence 95, App1
C 15	34	5.9	217	1	US-09-985-799-112	Sequence 112, App
C 16	34	5.9	217	1	US-08-594-031-112	Sequence 112, App
C 17	34	5.9	223	1	US-09-985-799-116	Sequence 116, App
C 18	34	5.9	223	1	US-08-594-031-116	Sequence 116, App
C 19	34	5.9	260	1	US-09-985-799-119	Sequence 119, App
C 20	34	5.9	260	1	US-08-594-031-119	Sequence 119, App
C 21	34	5.9	262	1	US-09-985-799-93	Sequence 93, App1
C 22	34	5.9	262	1	US-08-594-031-93	Sequence 93, App1
C 23	34	5.9	286	1	US-09-985-799-121	Sequence 121, App
C 24	34	5.9	286	1	US-08-594-031-121	Sequence 121, App
C 25	34	5.9	335	1	US-09-985-799-92	Sequence 92, App1
C 26	34	5.9	335	1	US-08-594-031-92	Sequence 92, App1
C 27	34	5.9	335	1	US-09-985-799-96	Sequence 96, App1
C 28	34	5.9	335	1	US-09-985-799-123	Sequence 123, App
C 29	34	5.9	335	1	US-08-594-031-92	Sequence 92, App1
C 30	34	5.9	335	1	US-08-594-031-94	Sequence 94, App1
C 31	34	5.9	335	1	US-08-594-031-96	Sequence 96, App1
C 32	34	5.9	335	1	US-08-594-031-123	Sequence 123, App
C 33	31	5.4	224	1	US-09-985-799-122	Sequence 122, App
C 34	31	5.4	224	1	US-08-594-031-122	Sequence 120, App
C 35	31	5.4	231	1	US-09-985-799-120	Sequence 120, App
C 36	31	5.4	231	1	US-08-594-031-120	Sequence 117, App
C 37	31	5.4	247	1	US-09-985-799-117	Sequence 117, App
C 38	31	5.4	247	1	US-08-594-031-117	Sequence 117, App
C 39	25	4.4	270	1	US-09-985-799-109	Sequence 109, App
C 40	25	4.4	270	1	US-08-594-031-109	Sequence 109, App
C 41	25	4.4	309	1	US-09-985-799-106	Sequence 106, App
C 42	25	4.4	309	1	US-08-594-031-106	Sequence 105, App
C 43	25	4.4	524	1	US-09-985-799-105	Sequence 105, App
C 44	25	4.4	524	1	US-08-594-031-105	Sequence 91, App1
C 45	16	2.8	2669	1	US-09-985-799-91	Sequence 91, App1

#### ALIGNMENTS

RESULT 1  
US-09-197-970B-4  
Sequence 4, Application US/09197970B  
Patent No. 6664385  
GENERAL INFORMATION:  
APPLICANT: Michele Santicola-Nadel  
Joseph V. Bonventre  
Catherine A. Hession  
Takaharu Ichimura  
Henry Wei  
Richard L. Cate

TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Biogen, Inc.  
STREET: 14 Cambridge Center  
CITY: Cambridge  
STATE: MA  
COUNTRY: USA

ZIP: 02142  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/197,970B  
FILING DATE: 23-NOV. 6664385-1998  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/018,228  
FILING DATE: 24-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Levine, Leslie W.  
REGISTRATION NUMBER: 35,245  
REFERENCE/DOCKET NUMBER: A010 PCT CIP



```

GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/985,799
FILING DATE: 06-NOV-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 04146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-985-799-111
Alignment Scores:
Pred. No.: 6.25e-33 Length: 335
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0
US-09-943-075a-2 (1-572) x US-09-985-799-111 (1-335)
QY 344 ProThrluSerThProSerProSerLeuMetProThrglyTyrlsSerMetGluLeu 363
DB 90 CCCACATTATCAACACCTAGCCCTCTTTAATGCTACTGTTACAAATCCATGAGAGTG 149
QY 364 SerAspIleSerAsnGluAsnCySArgIleAsnArgTyrgIlyrPhaArgAlaThrIle 383
DB 150 AGTGACATTTCGAATGAATACTGCCAATPAACAGATATGGCTACTTCAGAGCCACATC 209
QY 384 ThrIleVal 386
DB 210 ACAATGTGA 218
RESULT 3
US-08-594-031-111
; Sequence 111, Application US/08594031
; Patent No. 5783182
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```

GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 04146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-111
Alignment Scores:
Pred. No.: 6.25e-33 Length: 335
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0
US-09-943-075a-2 (1-572) x US-08-594-031-111 (1-335)
QY 344 ProThrluSerThProSerProSerLeuMetProThrglyTyrlsSerMetGluLeu 363
DB 90 CCCACATTATCAACACCTAGCCCTCTTTAATGCTACTGTTACAAATCCATGAGAGTG 149
QY 364 SerAspIleSerAsnGluAsnCySArgIleAsnArgTyrgIlyrPhaArgAlaThrIle 383
DB 150 AGTGACATTTCGAATGAATACTGCCAATPAACAGATATGGCTACTTCAGAGCCACATC 209
QY 384 ThrIleVal 386
DB 210 ACAATGTGA 218
RESULT 4
US-09-985-799-114/C
; Sequence 114, Application US/09985799
; Patent No. RE38392
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
```

```

NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,031
FILING DATE: 30-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 04146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-114

Alignment Scores:
Pred. No.: 6.6e-33 Length: 354
Score: 43.00 Matches: 43
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.52% Indels: 0
DB: 1 Gaps: 0

US-09-943-075A-2 (1-572) x US-08-594-031-114 (1-354)

QY 344 ProThleuSerThnProSerProSeIeuMeProThnGlyTyrIyVSeSerMetGluIeu 363
Db 139 CCCGACTTTCACACACCTACGCCCTCTTATGCTTACTGTTTCAATCATCAGAGCTG 80
QY 364 SerAsnIleSerAsnGluAnCysArgIleXenArgTyrGlyTyrPheArgAlaThrIle 383
Db 79 AGTACATTTCCATGAAACTGCGGATATACAGATATGCTACTTCAGAGCAACATC 20

QY 384 ThrIleVal 386
Db 19 ACAATTGTA 11

RESULT 6
US-09-985-799-115
Sequence 115, Application US/09985799
Patent No. R838392
GENERAL INFORMATION:
APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS, L.L.P.

```

STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 115:  
US-09-985-799-115  
Alignment Scores:  
Pred. No.: 8,76e-33 Length: 473  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.52% Indels: 0  
DB: 1 Gaps: 0  
US-09-943-075A-2 (1-572) x US-09-985-799-115 (1-473)  
QY 344 ProThriuserThProSerProSerLeuMetProThrglyTyrylyserMetGluLeu 363  
DB 218 CCCACATTCACACACCTGACCCCTCTTAATGCTACTGTTACCAATCCATGAGACTG 277  
QY 364 SerAspIleSerAsnGluAsnCyArgIleAsnArgTyrglyTyrrPheArgAlaThrIle 383  
DB 278 AGTGCATTTCCATGAATAAAGTCCGATTAACAGATATGCTACTTACGAGCCACCATC 337  
QY 384 ThrIleVal 386  
DB 338 ACAATTGTA 346  
RESULT 7  
US-08-594-031-115  
Sequence 115, Application US/08594031  
Patent No. 5783182  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BAKER & BOTTS, L.L.P.  
STATE: DC

STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX:  
INFORMATION FOR SEQ ID NO: 115:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 473 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-594-031-115  
Alignment Scores:  
Pred. No.: 8,76e-33 Length: 473  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.52% Indels: 0  
DB: 1 Gaps: 0  
US-09-943-075A-2 (1-572) x US-08-594-031-115 (1-473)  
QY 344 ProThriuserThProSerProSerLeuMetProThrglyTyrylyserMetGluLeu 363  
DB 218 CCCACATTCACACACCTGACCCCTCTTAATGCTACTGTTACCAATCCATGAGACTG 277  
QY 364 SerAspIleSerAsnGluAsnCyArgIleAsnArgTyrglyTyrrPheArgAlaThrIle 383  
DB 278 AGTGCATTTCCATGAATAAAGTCCGATTAACAGATATGCTACTTACGAGCCACCATC 337  
QY 384 ThrIleVal 386  
DB 338 ACAATTGTA 346  
RESULT 8  
US-09-985-799-113  
Sequence 113, Application US/09985799  
Patent No. RE38392  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSER: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 113:  
US-09-985-799-113  
Alignment Scores:  
Pred. No.: 1.14e-32 Length: 620  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.52% Indels: 0  
DB: 1 Gaps: 0  
US-09-943-075A-2 (1-572) x US-09-985-799-113 (1-620)  
QY 344 ProthleuserThrProSerProSerleuMetProthnglyTyTylyserMetGluLeu 363  
DB 218 CCACATTATCAACACCTAGCCCTCTTATGCTAGCTTACAATCCATGAGAGCTG 277  
QY 364 SerApplIeserAnGluAnGlyArgGlyLeuArgTyTyTyPheArgAlaThrIle 383  
DB 278 AGTGACATTTCATTAATAAACTGCCGATTAACAGATATGCTACTTCAGAGCCACATC 337  
QY 384 ThrIleVal 386  
DB 338 ACAATTGTA 346  
RESULT 9  
US-08-594-031-113  
Sequence 113, Application US/08594031  
Patent No. 5783182  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20004-2400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX:  
INFORMATION FOR SEQ ID NO: 113:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 620 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-594-031-113  
Alignment Scores:  
Pred. No.: 1.14e-32 Length: 620  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.52% Indels: 0  
DB: 1 Gaps: 0  
US-09-943-075A-2 (1-572) x US-08-594-031-113 (1-620)  
QY 344 ProthleuserThrProSerProSerleuMetProthnglyTyTylyserMetGluLeu 363  
DB 218 CCACATTATCAACACCTAGCCCTCTTATGCTAGCTTACAATCCATGAGAGCTG 277  
QY 364 SerApplIeserAnGluAnGlyArgGlyLeuArgTyTyTyPheArgAlaThrIle 383  
DB 278 AGTGACATTTCATTAATAAACTGCCGATTAACAGATATGCTACTTCAGAGCCACATC 337  
QY 384 ThrIleVal 386  
DB 338 ACAATTGTA 346  
RESULT 10  
US-09-383-586-27  
Sequence 27, Application US/09383586  
Patent No. 6242419  
GENERAL INFORMATION:  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevin  
APPLICANT: Orntust, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Marison, Greg  
TITLE OF INVENTION: Compounds isolated from stromal cells  
TITLE OF INVENTION: and methods for their use  
FILE REFERENCE: 11000.1037c1  
CURRENT APPLICATION NUMBER: US/09/383,586  
CURRENT FILING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 38  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 27  
LENGTH: 2213  
TYPE: DNA  
ORGANISM: Mouse  
US-09-383-586-27

Alignment Scores:  
Pred. No.: 3,96e-32 Length: 2213  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.52% Indels: 0  
DB: 3 Gaps: 0

US-09-943-075a-2 (1-572) x US-09-383-586-27 (1-2213)

Qy 344 ProthienseThProserProserLeuMetProthriGlyTyrIleSerMetGluLeu 363  
Db 1058 CCCGATTTCACACCTAGCCCTCTTTATGCTTACTGTACAAATTCATGAGCTG 1117

Qy 364 SeraspIleSerAsnGluAsnGlyArgIleAsnArgTyrGlyTyrPheArgAlaThrIle 383  
Db 1118 AGTGACATTTCCAAATGAAACTGCCGATTAACGATATGCTACTTCAGGCCACCATC 1177

Qy 384 ThrIleVal 386  
Db 1178 ACAATGTGA 1186

RESULT 11  
US-09-985-799-118  
Sequence 118, Application US/09985799  
Patent No. RE38392

GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/985,799  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: <Unknown>  
ORIGINAL SOURCE:  
SEQUENCE DESCRIPTION: SEQ ID NO: 118:  
US-09-985-799-118

Alignment Scores:  
Pred. No.: 2.98e-26 Length: 240  
Score: 36.00 Matches: 36  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.29% Indels: 0  
DB: 1 Gaps: 0

US-09-943-075a-2 (1-572) x US-09-985-799-118 (1-240)

Qy 82 LeuthySerAspSerProAlaLeuValGlySerAsnIleThrPheValValAsnLeuVal 101  
Db 39 CTGACGAGTACTACCCGCTCTGTGAGTTCACATATCACTTTGTGTGAACCTGGTG 98

Qy 102 PheProArgCysGlnIleGluAspAlaAsnGlyAsnIleValTyrGlu 117  
Db 99 TTCCCGAGATGCCAGAGGAGATGCTAATGCGATATGCTATAG 146

RESULT 12  
US-08-594-031-118  
Sequence 118, Application US/08594031  
Patent No. 5783182

GENERAL INFORMATION:  
APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BAKER & BOTTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2400

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/594,031  
FILING DATE: 30-JAN-1996  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/006,838  
FILING DATE: 16-NOV-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Remenick, James  
REGISTRATION NUMBER: 36,902  
REFERENCE/DOCKET NUMBER: 0A146-0110  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-639-7700  
TELEFAX: 202-639-7890  
TELEX:

INFORMATION FOR SEQ ID NO: 118:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 240 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-594-031-118

Alignment Scores:	2.1e-24	Length:	190
Pred. No.:		Matches:	34
Score:	34.00		

US-09-943-075A-2 (1-572) X US-08-594-031-95 (1-190)



QY 277 SerAlaIleSerTyrIysTyrPheAspPheGlyAspAsnThrGlyLeuPheValSerAsn 296  
DB 179 TCAGCATTTCTTCAAGAGTGAAGTCTTGAGGACACACTGAGCTGTGTTGCTCCACAAAT 120  
QY 297 HisThrLeuAsnHisThrTyrValLeuAsnGlyThrPheAsn 310  
DB 119 CACACTTGAATCACAATTATGTCCTCAATGAGACCTTCAAC 78

QY 297 HisThrLeuAsnHisThrTyrValLeuAsnGlyThrPheAsn 310  
DB 71 CACACTTGAATCACAATTATGTCCTCAATGAGACCTTCAAC 112  
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Job time: 128 secs

## RESULT 15

US-09-985-799-112  
Sequence 112, Application US/09985799  
Patent No. RE38392

## GENERAL INFORMATION:

APPLICANT: THOMPSON, Timothy C.  
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES  
NUMBER OF SEQUENCES: 175  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: BAKER & BOTS, L.L.P.  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004-2400

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/985,799

FILING DATE: 06-NOV-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/594,031

FILING DATE: 30-JAN-1996

APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0110

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-639-7700

TELEFAX: 202-639-7890

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 217 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: <Unknown>

ORIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 112:

## Alignment Scores:

Pred. No.:	2,39e-24	Length:	217
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.94%	Indels:	0
DB:	1	Gaps:	0

US-09-943-075a-2 (1-572) x US-09-985-799-112 (1-217)

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DB 11 TCAGCATTTCTTCAAGAGTGAAGTCTTGAGGACACACTGAGCTGTGTTGCTCCACAAAT 70

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 30, 2004, 17:46:50 ; Search time 577 Seconds  
(without alignments)  
4484.266 Million cell updates/sec

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Perfect score: 572  
Sequence: 1 MESLGVIVFLLAAGLEPLQ.....PFSRGREKDPDLQDKRMML 572

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Delop 6.0, Delext 7.0

Searched: 2936184 seqs, 2261732022 residues

Word size: 1

Total number of hits satisfying chosen parameters: 5864370

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Published Applications NA:  
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2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
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1	572	100.0	2320	9	US-09-943-075A-1	Sequence 1, Appl 1
2	141	24.7	631	17	US-10-404-460-129	Sequence 129, App
3	59	10.3	294	9	US-09-917-800A-139	Sequence 139, App
4	59	10.3	294	12	US-10-152-319A-122	Sequence 122, App
5	59	10.3	294	16	US-10-191-803-372	Sequence 372, App
6	43	7.5	2213	9	US-09-823-038A-27	Sequence 27, Appl
7	36	6.3	1725	9	US-09-943-075A-7	Sequence 7, Appl 1
8	21	3.7	65	10	US-09-908-975-1458	Sequence 1458, Ap
9	16	2.8	793	15	US-10-198-846-9201	Sequence 9201, Ap
10	16	2.8	1071	15	US-10-198-846-12825	Sequence 12825, A
11	16	2.8	1393	17	US-10-309-230-153	Sequence 153, App
12	16	2.8	1410	17	US-10-309-230-149	Sequence 149, App
13	16	2.8	1542	17	US-10-309-220-147	Sequence 147, App
14	16	2.8	1542	17	US-10-309-220-147	Sequence 147, App
15	16	2.8	1683	9	US-09-943-075A-8	Sequence 8, Appl 1
16	16	2.8	1923	17	US-10-309-290-151	Sequence 151, App
17	16	2.8	2661	13	US-10-463-106-1	Sequence 1, Appl 1
18	16	2.8	2661	14	US-10-039-272-1	Sequence 1, Appl 1
19	16	2.8	2666	15	US-10-084-817-169	Sequence 169, App
20	16	2.8	2669	10	US-09-525-978B-82	Sequence 82, Appl
21	16	2.8	2669	13	US-10-342-887-779	Sequence 779, App
22	16	2.8	2669	16	US-10-172-118-779	Sequence 779, App
23	16	2.8	2669	16	US-10-295-027-1041	Sequence 1041, Ap
24	16	2.8	2683	13	US-10-219-535-41	Sequence 41, App
25	16	2.8	2683	13	US-10-232-230-41	Sequence 41, App
26	16	2.8	2683	13	US-10-232-224-41	Sequence 41, App
27	16	2.8	2683	15	US-10-227-884-41	Sequence 41, App
28	16	2.8	2683	15	US-10-230-163-41	Sequence 41, App
29	16	2.8	2683	15	US-10-230-338-41	Sequence 41, App
30	16	2.8	2683	15	US-10-218-631-41	Sequence 41, App
31	16	2.8	2683	15	US-10-230-414-41	Sequence 41, App
32	16	2.8	2683	15	US-10-216-159A-41	Sequence 41, App
33	16	2.8	2683	15	US-10-218-849-41	Sequence 41, App
34	16	2.8	2683	15	US-10-227-873-41	Sequence 41, App
35	16	2.8	2683	15	US-10-227-883-41	Sequence 41, App
36	16	2.8	2683	15	US-10-219-076-41	Sequence 41, App
37	16	2.8	2683	15	US-10-230-434-41	Sequence 41, App
38	16	2.8	2683	15	US-10-219-003-41	Sequence 41, App
39	16	2.8	2683	15	US-10-219-075-41	Sequence 41, App
40	16	2.8	2683	15	US-10-219-464-41	Sequence 41, App
41	16	2.8	2683	15	US-10-219-466-41	Sequence 41, App
42	16	2.8	2683	15	US-10-219-479-41	Sequence 41, App
43	16	2.8	2683	15	US-10-219-481-41	Sequence 41, App
44	16	2.8	2683	15	US-10-230-260-41	Sequence 41, App
45	16	2.8	2683	15	US-10-232-231-41	Sequence 41, App

#### ALIGNMENTS

RESULT 1  
US-09-943-075A-1  
Sequence 1, Application US/09943075A  
Patent No. US20020151486A1  
GENERAL INFORMATION:  
APPLICANT: Popoff, Steven N.  
APPLICANT: Saifed, Reyes F.  
APPLICANT: Owen, Thomas A.  
APPLICANT: Smock, Steven L.  
TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,  
TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation  
FILE REFERENCE: 71369 263  
CURRENT APPLICATION NUMBER: US/09/943, 075A  
PRIOR FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: US 60/229, 006  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2320  
TYPE: DNA  
ORGANISM: Rat osteoactivin  
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (115)...(1833)
US-09-943-075A-1

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### Alignment Scores:

Pred. No.:	0	Length:	2320
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-943-075A-2 (1-572) X US-09-943-075A-1 (1-2320)

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Db	115	ATGGAAAGCTCTCGGGGGGCTGGGATTTCGTGCTGGCGAGGACGGCGCTCAG	174
Qy	21	AlAlaAlaYahgPhehTgaspValIeuGIYhiSGIuInTYrProAphIshEtArGIu	40
Db	175	GGCGCCAAACGGGATCCGTGATGGCTGGGCCCAAGAACATACCGGATCACTGAGGGAG	234
Qy	41	AsnAsnGIuLeuArGgIYrTPSerSeraspIuAsnGIuTPAspGIuInIeuTYrPro	60
Db	225	AACACCAATTACGTGGCTGTCTTCATATAAATGATGGATGAACGCTGATCCA	234
Qy	61	ValTrpArGArgIYgIuGIYArqTrpLYsAspSerTrpGIuGIYGIYArqValGIuAla	80
Db	295	GTGGAGAGAGAGGAGGAGGACATGAAAGACTCTGGGAAGAGGAGCGCTGGCGAGCA	354
Qy	81	AlaIleuThSerAspSerProAlaIeuValGIYSerAsnIleTrPheValIaIleu	100
Db	355	GGCTTACCAAGATTCACCGCGCTGGGTGGTCCAAATATACCTTGATGAGAACTGG	414
Qy	101	ValPheProArCYSGIuLYSGIuAspAlaAsnGIYAsnIleValTYrGIuArqAsnCYs	120
Db	415	GTGTGCCCAAGATGCGAAGAGAAATGCAAGCGCAATTCGTCTATGAGAGAACTGC	474
Qy	121	ArgSerAspLeuGIuLeuAlaSerAspProTYrValTYrAsnTrpThrGIYAlaAsp	140
Db	475	AGAAAGATTTTGAACCTGGCTCTGACCCGATCTCAACATGGACACAGGGGAGAC	534
Qy	141	AspGIuAspTrpGIuAspAsnTrsSerGIuGIYhIshIeLeuArgPheProAspGIYys	160
Db	535	GATAGAGACTGGGAAGACAAACACAGCCAGGCCAGCACTGAGTTCGCCAGCGGAG	594
Qy	161	ProPheProArgProhIshGIYArqLYsLYsTrpAsnPheValTYrValPhehIshIleu	180
Db	595	CCCTTCCTCGGCCCAAGACGGAAGAAATGGAACCTGCTCAAGTCTTCCACACACTT	654
Qy	181	GIYGIuInTYrPheGIuLYsLeuGIYGIuCYSerAlaArgValSerIleAsnTrpValAsn	200
Db	655	GGTAGATATTTCAAAACCTGGGTGCGAGTTCACAGAGTTTCATATAACAGAGTCAC	714
Qy	201	LeuThrValGIYProGIuInValMetGIuValIleValPheArgArgHishGIYArqAlaTYr	220
Db	715	TTGACATTTGGCCCTCAAGTCAAGAGTGTCTCTTCCGAAGACAGCGCGGGGATAC	774
Qy	221	IleProIleSerLYsValYsAspValTYrValIleThsAspGIuIleProIlePheVal	240
Db	775	ATTCCTCATCTCCAAAGATGAAGACGGTGTGTGATTAACATCAATCAATCCCTAATTCGGT	834
Qy	241	ThrMetTYrGIuLYsAsnAspArgAsnSerSeraspIuThrPheLeuArgAspLeuPro	260
Db	835	ACCATGTACCAAGAAATGACCGGAACGTGTGTATATAAAGCTTCTTCAGAGACTCCCGC	894
Qy	261	IlePhePheAspValIleuIleHishAspProSerHishPheLeuAsnTYrSerAlaIleSer	280
Db	895	ATTTCCTGATGATCCTCATTCACAGATCCCAATCATTTCTTCAACTCTGCACATTTCC	954
Qy	281	TYrLYsTrpAsnPhGIYAspAsnTrpGIYLeuPheValSerAsnAsnHishTrpLeuAsn	300
Db	955	TTCAGATGGAACTTTGGGGACACACTGGCTGGTTGTGTCCCAACATTCACACTTGGAT	1014

QY	301	HisThrTyrValIleuSmsIYThPheAspPheAsnLeuThrValGlnThAlaValPro	320
Db	1015	CAGAGTATGTCCTCAATGGAACTTAACTTTAACTCACTGCAACCTGCAAGTGGCG	1074
QY	321	GlyProCysProSerProThrThProSerProSerSerThrSerProSerProIAser	340
Db	1075	GAACATGAGCCCTCAACCAACCTTCCTCTCTTCTTGACTTCTCTTCCTCCGTCATCT	1134
QY	341	SerProSerProThrIleuSerThrProSerProSerIleuMetProThGlyTyrIlySser	360
Db	1135	TTCGCTTACCCACATTTATTCACACCTGAGCCCTCTTTAAAGCTCTAGGCTCAACAAATCC	1194
QY	361	MetGluIleuSerAspIleSerAsnGluAsnCysAspGlyIleAsnArgTyrGlyPheArg	380
Db	1195	ATGGAGCTGATGATCATTTTCATGATAAACTGGCCCAATAACAGATATGTTACTTCAG	1254
QY	381	AlaThrIleThrIleValIleAspGlyIleIleuGluValIleuIleIleGluValIleAspVal	400
Db	1255	GCACCATCATCAATTTGATGATGAATCCTTGAAGTCAACATCATCCAGGTGAGCAAGTCT	1314
QY	401	ProIleProThrIleuGlnProAspAsnSerIleuMetAspPheIleValThCysIlySgly	420
Db	1315	CCAAATCCCAACATGCAAGCTGACAACTCATGATGACTTCATGTGACCTGGAAAGGG	1374
QY	421	AlaThrProThrGluIleCysThrIleIleSerAspProThrCysGlnIleAlaGlnAsn	440
Db	1375	GCACCTCCAGGAAAGCTGTGACATCTCTGACCCCACTTCGCAGATGCCCAAGAAC	1434
QY	441	ArgValCysSerProValAlaValIleAspGluIleCysIleuSerValIleArgAlaPhe	460
Db	1435	AGGGGTGTGAGCCCGGTGGCTGTGGATGACCTGTGCTCTGCTCGTGGAGAGAGCCCTC	1494
QY	461	AsnGlySerGlyThrTyrCysValAsnPheThrIleuGlyAspAspAlaSerIleuAlaSer	480
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QY	481	ThrSerAlaIleuIleSerIleProGlyIlyAspIleuGlySerProIleuArgThValAsn	500
Db	1555	ACGAGGCGCTGATCTGTATCCCTGGCAAGACCTTAGGCTCCCTCTGAGAACAGTGAAT	1614
QY	501	GlyValIleuIleSerIleGlyCysIleuAlaMetPheValIleMetValThrIleIleuIleu	520
Db	1615	GGTGCTCCATATCCATTTGCTGCTGGCCCATGTTTGTCACAAAGTTCACATCTCTCTG	1674
QY	521	TyrIleValSerHleuSThrTyrIlySerProIleGlyAsnCysThrArgAsnValValIlyGly	540
Db	1675	TACAAAAAACACAGAGCGTACAGCAACATAGAACTGCACAGAGAACTGGTCAAGGCC	1734
QY	541	IlyGlyIlyeSerValPheIleuSerHsAlaIlyeAlaProPheSerArgGlyAspArgGlu	560
Db	1735	AAAGGCTGAGGTGTTTTTTCAGGCCATGCAAAAGCCCGCTTCCGAGAGACCGGAG	1794
QY	561	LysAspProIleuIleuGlnAspIlySerTrpMetIleu	572
Db	1795	AAGGATCCACTGCTCCAGGCAAGACCATGATGCTC	1830
RESULT 2			
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Sequence 129, Application US/10404460			
Publication No. US2004007697A1			
GENERAL INFORMATION:			
APPLICANT: PHASE-1 Molecular Toxicology, Inc.			
APPLICANT: Kier, Larry			
APPLICANT: Nolan, Timothy D.			
APPLICANT: Sarkar, Usha			
APPLICANT: Dertdel, Maher			
TITLE OF INVENTION: Liver Necrosis Predictive Genes			
FILE REFERENCE: 2874-022			
CURRENT APPLICATION NUMBER: US/10/404,460			
CURRENT FILING DATE: 2003-04-01			
PRIORITY APPLICATION NUMBER: US 66/369,287			
PRIORITY FILING DATE: 2002-04-01			

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PRIOR APPLICATION NUMBER: US 60/303,808  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/315,047  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: US 60/324,928  
PRIOR FILING DATE: 2001-09-27  
PRIOR APPLICATION NUMBER: US 60/330,867  
PRIOR FILING DATE: 2001-11-01  
PRIOR APPLICATION NUMBER: US 60/330,462  
PRIOR FILING DATE: 2001-10-22  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2221  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 122  
LENGTH: 294  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:  
OTHER INFORMATION: Genbank Accession No. AA851814  
US-10-152-319A-122

Alignment Scores:  
Pred. No.: 1,41e-51 Length: 294  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 10.31% Indels: 0  
DB: 12 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-152-319A-122 (1-294).

QY 359 LysSerMetGluLeuSerAspIleSerAsnGluAsnCysArgIleAsnArgTyrGlyTyr 378  
DB 294 AATCCATGAGCTGAGTGAATTCATGAACTGCGCAATTAACAGATATGGTTAC 235  
QY 379 PheArgAlaThrIleThrIleValAspGlyIleLeuGluValAsnIleIleGlnValAla 398  
DB 234 TTCAGAGCCACCATCCATCTTGAATGTAATCTTGAAAGTCAACATCATCCAGGTAGCA 175  
QY 399 AspValProIleProThrLeuGlnProAspAsnSerLeuMetAspPheIleValThr 417  
DB 174 GATGTCCCAATCCCACTGACGCTGACACACTCATCTGATGACTTGTGACC 118

## RESULT 5

US-10-191-803-372/C  
Sequence 372, Application US/10191803  
Publication No. US20040014040A1  
GENERAL INFORMATION:  
APPLICANT: MENDRICK, Donna  
APPLICANT: PORTER, Mark  
APPLICANT: JOHNSON, Kory  
APPLICANT: HIGGS, Brandon  
APPLICANT: CASTLE, Arthur  
APPLICANT: ELASHOFF, Michael  
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling  
FILE REFERENCE: 44921-5090US  
CURRENT APPLICATION NUMBER: US/10/191,803  
CURRENT FILING DATE: 2002-07-10  
PRIOR APPLICATION NUMBER: US 60/303,819  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/305,623  
PRIOR FILING DATE: 2001-07-17  
PRIOR APPLICATION NUMBER: US 60/369,351  
PRIOR FILING DATE: 2002-04-03  
PRIOR APPLICATION NUMBER: US 60/377,611  
NUMBER OF SEQ ID NOS: 1140  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 372  
LENGTH: 294  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
FEATURE:

OTHER INFORMATION: Genbank Accession No. US20040014040A1 AA851814  
US-10-191-803-372

Alignment Scores:  
Pred. No.: 1,41e-51 Length: 294  
Score: 59.00 Matches: 59  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 10.31% Indels: 0  
DB: 16 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-191-803-372 (1-294)

QY 359 LysSerMetGluLeuSerAspIleSerAsnGluAsnCysArgIleAsnArgTyrGlyTyr 378  
DB 294 AATCCATGAGCTGAGTGAATTCATGAACTGCGCAATTAACAGATATGGTTAC 235  
QY 379 PheArgAlaThrIleThrIleValAspGlyIleLeuGluValAsnIleIleGlnValAla 398  
DB 234 TTCAGAGCCACCATCCATCTTGAATGTAATCTTGAAAGTCAACATCATCCAGGTAGCA 175  
QY 399 AspValProIleProThrLeuGlnProAspAsnSerLeuMetAspPheIleValThr 417  
DB 174 GATGTCCCAATCCCACTGACGCTGACACACTCATCTGATGACTTGTGACC 118

## RESULT 6

US-09-823-038A-27  
Sequence 27, Application US/09823038A  
Patent No. US20020058335A1  
GENERAL INFORMATION:

APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevin  
APPLICANT: Onrust, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Marison, Greg  
TITLE OF INVENTION: Compositions Isolated From Stromal Cells  
FILE REFERENCE: 11000.103763  
CURRENT APPLICATION NUMBER: US/09/823,038A  
CURRENT FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 27  
LENGTH: 2213  
TYPE: DNA  
ORGANISM: Mouse  
US-09-823-038A-27

Alignment Scores:  
Pred. No.: 3.95e-34 Length: 2213  
Score: 43.00 Matches: 43  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 7.52% Indels: 0  
DB: 9 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-823-038A-27 (1-2213)

QY 344 ProThrLeuSerThrProSerProSerLeuMetProThrGlyTyrLysSerMetGluLeu 363  
DB 1058 CCAACATTTACACCTACCTCCCTTTATGCTACCTGTTACAAATCAAGAGGCTG 1117  
QY 364 SerAspIleSerAsnGluAsnCysArgIleAsnArgTyrGlyTyrPheArgAlaThrIle 383  
DB 1118 AGTGAATTCATCCAGAAATCGCAATATAACGATATGCTACTTCAAGACCAATC 1177  
QY 384 ThrIleVal 386  
DB 1178 ACAATTGA 1186

## RESULT 7

US-09-943-075A-7

Sequence 7, Application US/09943075A  
Patent No. US20020151486A1  
GENERAL INFORMATION:  
APPLICANT: Popoff, Steven N.  
APPLICANT: Safado, Favez F.  
APPLICANT: Owen, Thomas A.  
APPLICANT: Smock, Steven L.  
TITLE OF INVENTION: Osteocalcin Protein and Nucleic Acids Encoding the Same,  
FILE REFERENCE: 71369.262  
CURRENT APPLICATION NUMBER: US/09/943,075A  
CURRENT FILING DATE: 2001-08-30  
PRIOR APPLICATION NUMBER: US 60/229,006  
PRIOR FILING DATE: 2000-08-30  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 7  
LENGTH: 1725  
TYPE: DNA  
ORGANISM: Mouse  
US-09-943-075A-7

Alignment Scores:  
Pred. No.: 5 81e-27 Length: 1725  
Score: 36.00 Matches: 36  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 6.29% Indels: 0  
DB: 9 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-943-075A-7 (1-1725)

Qy 82 LeuThSeAspSePProAlaLeuValGlySeAenIeThrPheValValAsnLeuVal 101  
Db 244 CTGACCGATGACTCACCGGCTCTGGGGTTCATATACCTTTGTGGTGAACCTGTTG 303

Qy 102 PheProArGyGslInyGsluAspAlaAsnGlyAsnIleValTYrGlu 117  
Db 304 TTCCCGAGATGCCAAGAGAGATGCTAATGCAATATGCTATGAG 351

RESULT 8  
US-09-908-975-1458  
Sequence 1458, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: WASSERMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: MINTZ, Liat  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1458  
LENGTH: 65  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-09-908-975-1458

Alignment Scores:  
Pred. No.: 9.95e-13 Length: 65  
Score: 21.00 Matches: 21  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 3.67% Indels: 0

DB: 10 Gaps: 0

US-09-943-075A-2 (1-572) x US-09-908-975-1458 (1-65)

Qy 258 AspleuProIlePhePheAspValLeuIleHisAspProSerHisPheLeuAntySer 277  
Db 3 GACCTCCCATTTTCTTGATGCTCCTCATTCACATCCAGTATCTTCTCACTACTCT 62

Qy 278 Ala 278  
Db 63 GCC 65

RESULT 9  
US-10-198-846-9201  
Sequence 9201, Application US/10198846  
Publication No. US20030099974A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Xu, Yongyao  
APPLICANT: Wang, Youzhen  
APPLICANT: Steinmann, Kathleen  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MRI-049  
CURRENT APPLICATION NUMBER: US/10/198,846  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/306,220  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14084  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9201  
LENGTH: 793  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 7..11, 21, 590, 602, 617, 686, 703, 725, 738, 793  
OTHER INFORMATION: n = A,T,C or G  
US-10-198-846-9201

Alignment Scores:  
Pred. No.: 1.65e-06 Length: 793  
Score: 16.00 Matches: 16  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 2.80% Indels: 0  
DB: 15 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-198-846-9201 (1-793)

Qy 102 PheProArGyGslInyGsluAspAlaAsnGlyAsnIleValTYrGlu 117  
Db 405 TTCCCTAGATGCCAAGAGAGATGCCAATGCAATATGCTATGAG 452

RESULT 10  
US-10-198-846-12825  
Sequence 12825, Application US/10198846  
Publication No. US20030099974A1  
GENERAL INFORMATION:  
APPLICANT: Lillie, James  
APPLICANT: Xu, Yongyao  
APPLICANT: Wang, Youzhen  
APPLICANT: Steinmann, Kathleen  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
FILE REFERENCE: MRI-049  
CURRENT APPLICATION NUMBER: US/10/198,846  
CURRENT FILING DATE: 2002-07-18  
PRIOR APPLICATION NUMBER: 60/306,220  
PRIOR FILING DATE: 2001-07-18  
NUMBER OF SEQ ID NOS: 14084

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12825
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1070..1071
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-12825

Alignment Scores:
Pred. No.: 2.2e-06 Length: 1071
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.80% Indels: 0
DB: 15 Gaps: 0

US-09-943-075a-2 (1-572) x US-10-198-846-12825 (1-1071)

QY 102 PheProArgCysGlnIlySGlnAspAlaAsnGlyAsnIleValTyrGln 117
Db 459 TTCCTAGATGCCAAAAGAGATGCCAATGCGACATATGCTATGAG 506

RESULT 11
US-10-309-290-153
; Sequence 153, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/348,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
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; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 153
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDG
; LOCATION: (2)..(1393)
US-10-309-290-153

Alignment Scores:
Pred. No.: 2.82e-06 Length: 1393
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.80% Indels: 0
DB: 17 Gaps: 0

US-09-943-075a-2 (1-572) x US-10-309-290-153 (1-1393)

QY 102 PheProArgCysGlnIlySGlnAspAlaAsnGlyAsnIleValTyrGln 117
Db 248 TTCCTAGATGCCAAAAGAGATGCCAATGCGACATATGCTATGAG 295

RESULT 12
US-10-309-290-149
; Sequence 149, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
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; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 149
; LENGTH: 1410
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1410)
US-10-309-290-149

Alignment Scores:
Pred. No.: 2.85e-06 Length: 1410
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.80% Indels: 0
DB: 17 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-309-290-149 (1-1410)
QY 102 PheProArgCysGlnIleGluAspAlaAsnGlyAsnIleValTyrGlu 117
Db 238 TTCCTGATGATGCCAAAGAGAGATGCCATGCGACATGATGCTATGAG 285

RESULT 13
US-10-309-290-147
; Sequence 147, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsodrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Edinger, Shomik R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rochberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
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; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Wei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 147
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1542)
US-10-309-290-147

Alignment Scores:
Pred. No.: 3.1e-06 Length: 1542
Score: 16.00 Matches: 16
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.80% Indels: 0
DB: 17 Gaps: 0

US-09-943-075A-2 (1-572) x US-10-309-290-147 (1-1542)
QY 102 PheProArgCysGlnIleGluAspAlaAsnGlyAsnIleValTyrGlu 117
Db 238 TTCCTGATGATGCCAAAGAGAGATGCCATGCGACATGATGCTATGAG 285

RESULT 14
US-09-943-075A-8
; Sequence 8, Application US/09943075A
; Patent No. US20020151486A1
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Fayer F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteocytic Protein and Nucleic Acids Encoding the Same,
; TITLE OF INVENTION: Compositions and Methods of Stimulating Bone Differentiation
; FILE REFERENCE: 71369,262
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1683
; TYPE: DNA
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ORGANISM: Human  
US-09-943-075A-8

Alignment Scores:

Pred. No.:	3,37e-06	Length:	1683
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.80%	Indels:	0
DB:	9	Gaps:	0

US-09-943-075A-2 (1-572) x US-09-943-075A-8 (1-1683)

Qy 102 PheProArgCysGlnIysGluAapAlaasnGlyAsnIleValTyrGlu 117  
Db 304 TTCCTAGATGCCAAAGAGATGCCAATGCGCAACATATGCTATGAG 351

RESULT 15  
US-10-309-290-151

Sequence 151, Application US/10309290  
Publication No. US20040023241A1  
GENERAL INFORMATION:

APPLICANT: Alsobrook II, John P.  
APPLICANT: Anderson, David W.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Chilikuru, Rajeev A.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gerlach, Valerie L.  
APPLICANT: Gorman, Linda  
APPLICANT: Gould-Rothberg, Bonnie E.  
APPLICANT: Guo, Xiaojia  
APPLICANT: Jeffers, Michael E.  
APPLICANT: Ji, Weizhen  
APPLICANT: Li, Li  
APPLICANT: Malvanekar, Uriel M.  
APPLICANT: Miller, Charles E.  
APPLICANT: Murphy, Ryan  
APPLICANT: Paturajan, Meera  
APPLICANT: Peyman, John A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Rieser, Daniel K.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Smithson, Glenda  
APPLICANT: Scaring, Gary  
APPLICANT: Taupier, Raymond J.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zhong, Haihong  
APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

FILE REFERENCE: 21402-502A  
CURRENT APPLICATION NUMBER: US/10/309,290  
CURRENT FILING DATE: 2002-12-02  
PRIOR APPLICATION NUMBER: 60/336,600  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: 60/338,285  
PRIOR FILING DATE: 2001-12-07  
PRIOR APPLICATION NUMBER: 60/341,346  
PRIOR FILING DATE: 2001-12-12  
PRIOR APPLICATION NUMBER: 60/341,477  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/341,540  
PRIOR FILING DATE: 2001-12-17  
PRIOR APPLICATION NUMBER: 60/342,592  
PRIOR FILING DATE: 2001-12-20  
PRIOR APPLICATION NUMBER: 60/344,297  
PRIOR FILING DATE: 2001-12-27  
PRIOR APPLICATION NUMBER: 60/344,903  
PRIOR FILING DATE: 2001-12-31  
PRIOR APPLICATION NUMBER: 60/373,288  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 60/380,981  
PRIOR FILING DATE: 2002-05-15

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 274  
SOFTWARE: Cnaseqdist version 0.1  
SEQ ID NO 151  
LENGTH: 1923  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (95)..(1774)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(1)  
OTHER INFORMATION: wherein n may be a, c, g or t  
NAME/KEY: misc feature  
LOCATION: (3)..(3)  
OTHER INFORMATION: wherein n may be a, c, g or t  
US-10-309-290-151

Alignment Scores:

Pred. No.:	3.82e-06	Length:	1923
Score:	16.00	Matches:	16
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.80%	Indels:	0
DB:	17	Gaps:	0

US-09-943-075A-2 (1-572) x US-10-309-290-151 (1-1923)

Qy 102 PheProArgCysGlnIysGluAapAlaasnGlyAsnIleValTyrGlu 117  
Db 398 TTCCTAGATGCCAAAGAGATGCCAATGCGCAACATATGCTATGAG 445

Search completed: April 30, 2004, 19:21:49  
Job time : 586 secs